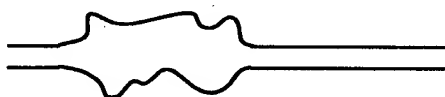
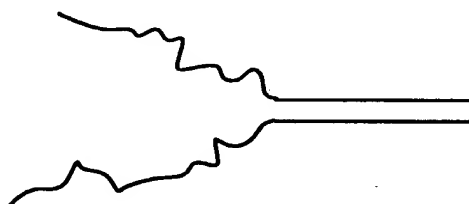


1/23

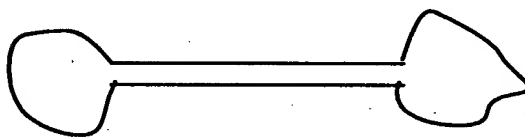
(A)



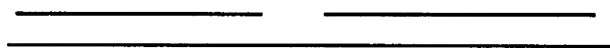
(B)



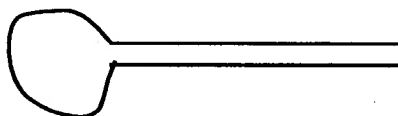
(C)



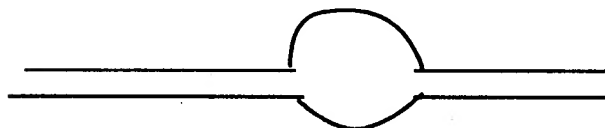
(D)



(E)

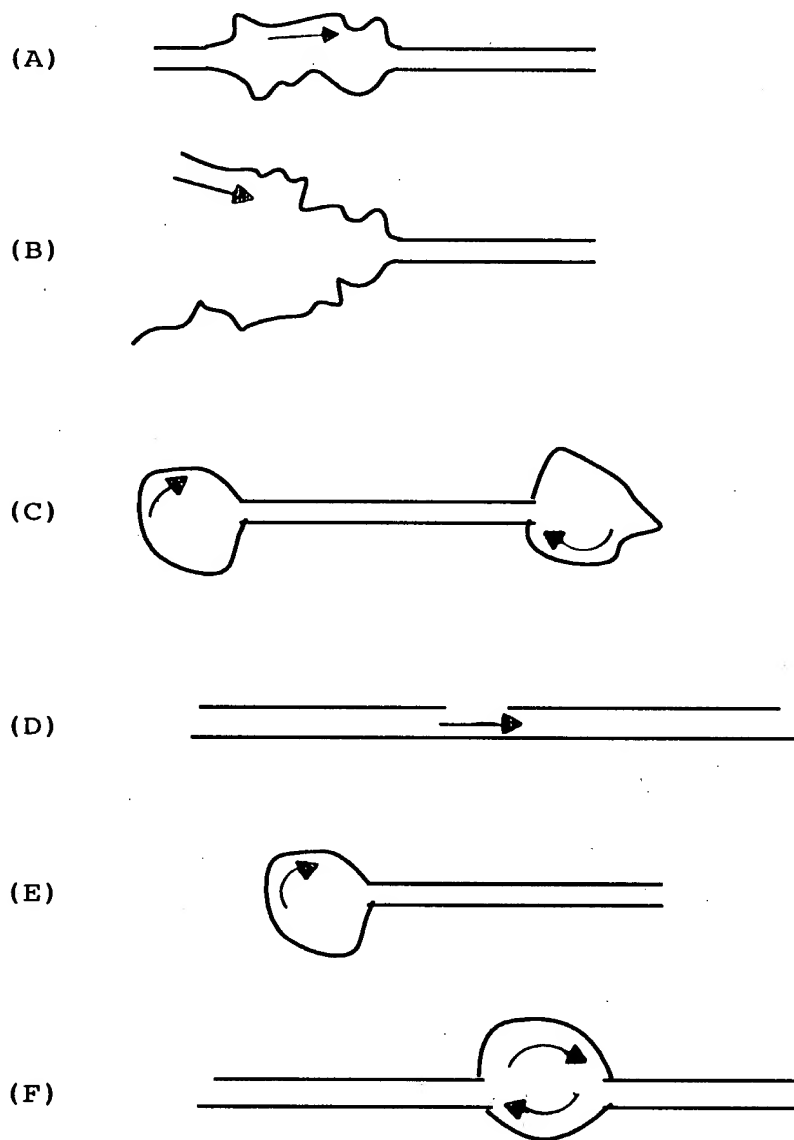


(F)

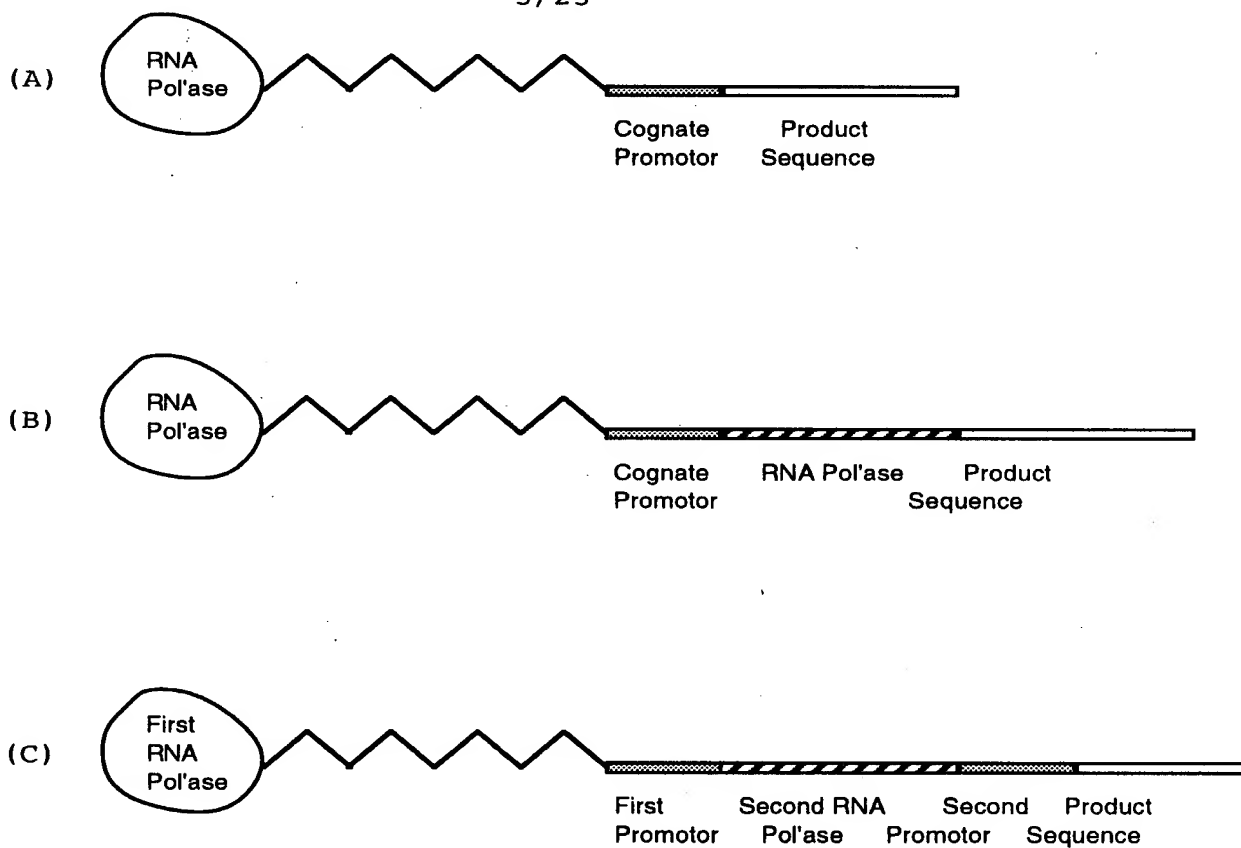
**Figure 1 (A-F)**

**Construct Forms Comprising at Least one Single-Stranded
Region**

2/23

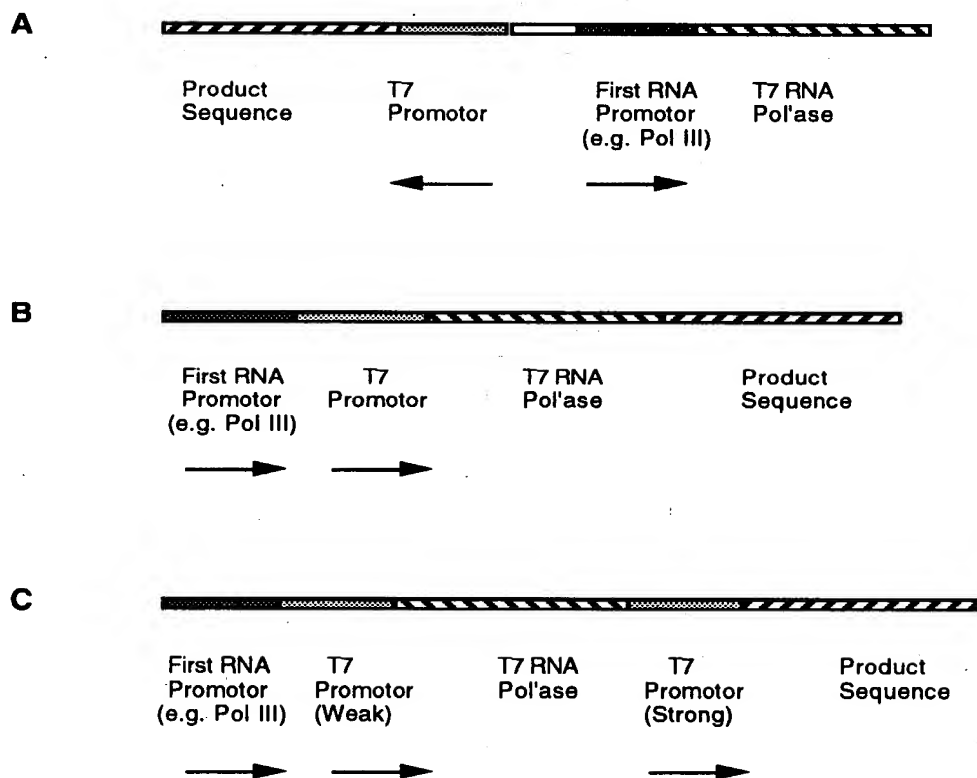
**Figure 2 (A-F)****Functional Forms of the Construct**

3/23

**Figure 3 (A-C)**

**Three Constructs with an RNA Polymerase
Covalently Attached to a Transcribing Cassette**

4/23

**Figure 4 (A-C)**

**Three Constructs with Promoters
for Endogenous RNA Polymerase**

M13mp18. Seq Length: 7250

1.	AATGCTACTA	CTATTAGTAG	AATTGATGOC	ACCTTTTCAG	CTOGOGOOOC
51.	AAATGAAAAT	ATAGCTAAAC	AGGTTATTGA	OCATTTGCGA	AATGTATCTA
101.	ATGGTCAAAC	TAAATCTACT	OGTTGCGAGA	ATTGGGAATC	AACTGTTACA
151.	TGGAATGAAA	CTTCCAGACA	COGTACTTTA	GTTGCATATT	TAAAACATGT
201	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGOCA	TOOGCAAAAA
251	TGAOCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TOCTGAOCTG
301.	TTGGAGTTTG	CTTCCGGTCT	GGTTGCTTTT	GAAGCTOGAA	TTAAAAOGOG
351.	ATATTTGAAG	TCTTTGGGGC	TTCTCTTTAA	TCTTTTTGAT	GCAATCOGCT
401.	TTGCTTCTGA	CTATAATAGT	CAGGGTAAAG	AOCTGATTTT	TGATTTATGG
451.	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	TTTGAGGGGG	ATTCAATGAA
501.	TATTTATGAC	GATTOGCAG	TATTGGAOCG	TATCCAGTCT	AAACATTTTA
551.	CTATTACOOO	CTCTGGCAAA	ACTTCTTTTG	CAAAAGOCTC	TOGCTATTTT
601.	GGTTTTTATC	GTOGTCTGGT	AAAOGAGGGT	TATGATAGTG	TTGCTCTTAC
651.	TATGOCTCGT	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG
701.	GTATTCCTAA	ATCTCAACTG	ATGAATCTTT	CTAOCTGTAA	TAATGTTGTT
751.	COGTTAGTTC	GTTTTATTAA	CGTAGATTTT	TCTTCCCAAC	GTOCTGACTG
801.	GTATAATGAG	CCAGTTCTTA	AAATGCGATA	AGGTAATTCA	CAATGATTAA
851.	AGTTGAAATT	AAACCATCTC	AAGOOCAATT	TACTACTOGT	TCTGGTGTTT
901.	TOGTCAGGGC	AAGCTTATT	CACTGAATGA	GCAGCTTTGT	TACGTTGATT
951.	TGGGTAATGA	ATATCOGGTT	CTTGTOGAAG	ATTACTCTTG	ATGAAGGTCA
1001	GOCAGOCAT	GOGOCGGTC	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG
1051	TTGGTCAGTT	CGGTTCCCTT	ATGATTGAOC	GTCTGOGOC	OGTTCCGGCT
1101	AAGTAACATG	GAGCAGGTGG	CGGATTTGGA	CACAATTTAT	CAGGOGATGA
1151	TACAAATCTC	CGTTGTACCT	TGTTTGGGGC	TTGGTATAAT	OGCTGGGGGT
1201	CAAAGATGAG	TGTTTTAGTG	TATTCTTTGG	OCTCTTTGGT	TTTAGGTTGG

Figure 5

M13mp18 Nucleic Acid Sequence

6/23

1251	TGOCCTGTA	GTGGCATTAC	GTATTTTACC	OGTTTAATGG	AAACTTCTC
1301	ATGAAAAAGT	CTTTAGTCCT	CAAAGCCTCT	GTAGOOGTG	CTAOCCTCGT
1351	TOOGATGCTG	TCTTTOGCTG	CTGAGGGTGA	OGATOOOGCA	AAAGOGGGOCT
1401	TTAACTOOC	GCAAGCCTCA	GOGAOCGAAT	ATATCGGTTA	TGOGTGGGOG
1451	ATGGTTGTTG	TCATTGTGG	OGCAACTATC	GGTATCAAGC	TGTTTAAGAA
1501	ATTCACCTOG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT
1551	GGAGOCCTTT	TTTTTGGA	TTTCAACGT	GAAAAAATTA	TTATTCGCAA
1601	TTCCTTTAGT	TGTTCTTTC	TATTCTCACT	COGCTGAAAC	TGTTGAAAGT
1651	TGTTTAGCAA	AAOCCATAC	AGAAAATTCA	TTACTAACG	TCTGGAAAGA
1701	OGACAAAAC	TTAGATCGTT	AOGCTAACTA	TGAGGGTTGT	CTGTGGAATG
1751	CTACAGGOGT	TGTAGTTTGT	ACTGGTGAOG	AAACTCAGTG	TTACGGTACA
1801	TGGGTTCTA	TTGGGCTTGC	TATCOCTGAA	AATGAGGGTG	GTGGCTCTGA
1851	GGGTGGGGT	TCTGAGGGTG	GOGGTTCTGA	GGGTGGGGT	ACTAAACCTC
1901	CTGAGTAOGG	TGATACAOC	ATTOGGGGCT	ATACTTATAT	CAOCCCTCTC
1951	GAOGGCACTT	ATOOGCCTGG	TACTGAGCAA	AAOOGCTA	ATCCTAATOC
2001	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	CAGAATAATA
2051	GGTTOOGAAA	TAGGCAGGGG	GCATTAAC	TTTATAOGGC	CACTGTTACT
2101	CAAGGCACTG	AOCCOGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC
2151	AAAAGOCATG	TATGACGCTT	ACTGGAAOGG	TAAATTCAGA	GACTGOGCTT
2201	CAAGGCACTG	AOCCOGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC
2151	AAAAGOCATG	TGOCCTCAAC	TOCTGTCAAT	GCTGGGGGGG	GCTCTGGTGG
2201	TOCATCTGG	CTTTAATCAA	GATOCATTOG	TTTGTGAATA	TCAAGGOC
2251	TOGTCTGAOC	TGOCCTCAAC	TOCTGTCAAT	GCTGGGGGGG	GCTCTGGTGG
2301	TGGTTCTGGT	GGGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	GGGGTTCTG
2351	AGGGTGGGG	CTCTGAGGGA	GGGGTTTOG	GTGGTGGCTC	TGGTTOGGT
2401	GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGAOOGA
2451	AAATGOOGAT	GAAAACGGGC	TACAGTCTGA	OGCTAAAGGC	AAACTTGATT

Figure 5

M13mp18 Nucleic Acid Sequence

7/23

2501	CTGTGCTAC	TGATTACGGT	GCTGCTATOG	ATGGTTTCAT	TGGTGAOGTT
2551	TOGGGOCITG	CTAATGGTAA	TGGTGCTACT	GGTGATTTTG	CTGGCTCTAA
2601	TTCCCAAATG	GCTCAAGTOG	GTGAOGGTGA	TAATTCAOCT	TTAATGAATA
2651	ATTTCOGTCA	ATATTTACCT	TOOCTOOCTC	AATOGGTTGA	ATGTGGOOCT
2701	TTTGTCTTTA	GOGCTGGTAA	AOCATATGAA	TTTTCTATTG	ATTGTGACAA
2751	AATAAACTTA	TTOOGTGGTG	TCTTTGOGTT	TCTTTTATAT	GTTGOCACCT
2801	TTATGTATGT	ATTTTCTACG	TTTGCTAACA	TACTGOGTAA	TAAGGAGTCT
2851	TTATCATGOC	AGTTCTTTTG	GGTATTOOGT	TATTATTGCG	TTTOCTOGGT
2901	TTOCTTCTGG	TAACTTTGTT	CGGCTATCTG	CTTACTTTTC	TTAAAAAGGG
2951	CTTOGGTAAG	ATAGCTATTG	CTATTTCAAT	GTTTCTTGCT	CTTATTATTG
3001	GGCTTAACTC	AATTCTTG TG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA
3051	COCTCTGACT	TTGTTCAAGG	TGTTCAAGTTA	ATTCTCOOGT	CTAATGOGCT
3101	TCOCTGTTTT	TATGTTATTC	TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG
3151	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	ATTGGGATAA	ATAATATGGC
3201	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGAOG	CTOGTTAGOG
3251	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT
3301	CTTGATTTAA	GGCTTCAAAA	OCTCOOGCAA	GTOGGGAGGT	TOGCTAAAAC
3351	GCTOGOGITT	CTTAGAATAC	OGGATAAGOC	TTCTATATCT	GATTTGCTTG
3401	CTATTGGGOG	CGGTAATGAT	TOCTACGAATG	AAAATAAAAA	CGGCTTGCTT
3451	GTTCTOGATG	AGTGOGGTAC	TTGGTTTAAT	AOCO GTTCTT	GGAATGATAA
3501	GGAAAGACAG	COGATTATTG	ATTGGTTTCT	ACTGCTOGT	AAATTAGGAT
3551	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGOG
3601	OGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTOGTGCTC	TGGACAGAAT
3651	TACTTTAOCT	TTTGTOGGTA	CTTTATATTC	TCTTATTACT	GGCTOGAAAA
3701	TGOCTCTGOC	TAAATTACAT	GTTGGOGTTG	TTAAATATGG	OGATTCTCAA
3751	TTAAGOOCTA	CTGTTGAGOG	TTGGCTTTAT	ACTGGTAAGA	ATTTGTATAA
3801	OGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	TOCGGTGTTT

Figure 5

3851	ATTCTTATTT	AACGCCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA
3901	AATTTAGGTC	AGAAGATGAA	ATTAACATAA	ATAATATTGA	AAAAGTTTTC
3951	TOGOGTTCTT	TGTCTTGCGA	TTGGATTGTC	ATCAGCATT	ACATATAGTT
4001	ATATAACCCA	AOCTAAGCOG	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT
4051	GATTTTGATA	AATTCACAT	TGACTCTTCT	CAGOGTCTTA	ATCTAAGCTA
4101	TOGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	AGOGAOGATT
4151	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC
4201	ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT
4251	TCTTGATGTT	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT
4301	AATTOGCTC	TGOGOGATTT	TGTAACCTGG	TATTCAAAGC	AATCAGGOGA
4351	AATOCGTTATT	GTTTCTOOOG	ATGTAAAAGG	TACTGTTACT	GTATATTCAT
4401	CTGACGTTAA	AOCTGAAAAT	CTACGCAATT	TCTTTATTTT	TGTTTTACGT
4451	GCTAATAATT	TTGATAATGGT	TGGTTCAATT	OCTTOCATAA	TTCAGAAGTA
4501	TAATOCAAAC	AATCAGGATT	ATATTGATGA	ATTGOCATCA	TCTGATAATC
4551	AGGAATATGA	TGATAATTCC	GCTOCTTCTG	GTGGTTTCTT	TGTTTOGCAA
4601	AATGATAATG	TACTCAAAC	TTTTAAAATT	AATAACGTTT	GGGCAAAGGA
4651	TTAATAACGA	GTTGTGGAAT	TGTTTGTAAG	GTCTAATACT	TCTAAATCCT
4701	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	TAGTGCTCCT
4751	AAAGATATTT	TAGATAAOC	TOCTCAATTC	CTTTCTACTG	TTGATTTGOC
4801	AACTGAOCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG
4851	ATGCTTTAGA	TTTTTCATTT	GCTGCTGGCT	CTCAGOGTGG	CACTGTTGCA
4901	GGOGGTGTTA	ATACTGACOG	OCTCAOCTCT	GTTTTATCTT	CTGCTGGTGG
4951	TTOGTTGGGT	ATTTTAAATG	GOGATGTTTT	AGGGCTATCA	GTTOGOGCAT
5001	TAAAGACTAA	TAGOCATTCA	AAAATATTGT	CTGTGOCACG	TATTCTTAOC
5051	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGOCAGAATG	TCOCTTTTAT
5101	TAAAGACTAA	TAGOCATTCA	AAAATATTGT	CTGTGOCACG	TATTCTTAOC
5151	OGATTGAGOG	TCAAAATGTA	GGTATTTCCA	TGAGOGTTTT	TOCTGTTGCA

Figure 5

9/23

5201	ATGGCTGGOG	GTAATATTGT	TCTGGATATT	AOCAGCAAGG	CCGATAGTTT
5251	GAGTTCTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA	AGAAGTATTG
5301	CTACAAOGGT	TAATTTGOGT	GATGGACAGA	CTCTTTTACT	OGGTGGOOCTC
5351	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGOGTAOOGT	TOCTGTCTAA
5401	AATCOCTTTA	ATOGGOCTOC	TGTTTAGCTC	OOGCTCTGAT	TOCAAOGAGG
5451	AAAGCAOGTT	ATAOGTGCTC	GTCAAAGCAA	OCATAGTAOG	OGOOCTGTAG
5501	OGGOGCATT	AGOGGGGGG	GTGTGGTGGT	TAOGOGCAGC	GTGAOOGCTA
5551	CACTTGOCAG	OGOOCTAGOG	OOOGCTOCTT	TCGCTTTCTT	COCTTCOCTT
5601	CTOGOCAOGT	TOGOOGGCTT	TOOOOGTCAA	GCTCTAAATC	GGGGGCTOOC
5651	TTAGGGTTC	OGATTTAGTG	CTTTACGGCA	OCTOGAOOOC	AAAAAACTTG
5701	ATTTGGGTGA	TGGTTCAOGT	AGTGGGOCAT	OGOOCTGATA	GAOGGTTTTT
5751	OGOOCTTTGA	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTOCA
5801	AACTGGAACA	ACACTCAAOC	CTATCTOGGG	CTATTCTTTT	GATTTATAAG
5851	GGATTTTGOC	GATTTOGGAA	OCACCATCAA	ACAGGATTTT	OGOOTGCTGG
5901	GGCAAOCAG	CGTGGAOOGC	TTGCTGCAAC	TCTCTCAGGG	OCAGGOGGTG
5951	AAGGGCAATC	AGCTGTTGOC	OGTCTOGCTG	GTGAAAAGAA	AAAOCAOOCT
6001	GGOGOOCAAT	AOGCAAAOOG	OCTCTOOOOG	OGOGTTGGOC	GATTCATTAA
6051	TGCAGCTGGC	AOGACAGGTT	TOOOGACTGG	AAAGOGGGCA	GTGAGOGCAA
6101	CGCAATTAAT	GTGAGTTAGC	TCACTCATT	GGCAOOOCAG	GCTTTACACT
6151	TTATGCTTCC	GGCTOGTATG	TTGTGTGGAA	TTGTGAGOGG	ATAACAATTT
6201	CACACAGGAA	ACAGCTATGA	OCATGATTAC	GAATTOGAGC	TOGGTAOOOG
6251	GOGATOCTCT	AGAGTOGAOC	TGCAGGCATG	CAAGCTTGGC	ACTGGOOGTG
6301	GTTTTACAAC	GTOGTGACTG	GGAAAACOOCT	GGOGTTAOC	AACTTAATOG
6351	OCTTGACGCA	CAATCOOCTT	TOGOCAGCTG	GOGTAATAGC	GAAGAGGOOC
6401	GCAOOGATOG	COCTTOCCAA	CAGTTGOGCA	GOCTGAATGG	OGAATGGOGC
6451	TTTGOCTGGT	TTOOGGCAOC	AGAAGOGGTG	COGGAAAGCT	GGCTGGAGTG
6501	CGATCTTCT	GAGGOCGATA	CGTGTGTGT	COOCTCAAAC	TGGCAGATGC

Figure 5

M13mp18 Nucleic Acid Sequence

10/23

6551	ACGGTTAOGA	TGOGCOOCATC	TACACCAACG	TAAOCTATOC	CATTAOGGTC
6601	AATOOGCOGT	TTGTTCCOCAC	GGAGAATCOG	ACGGGTTGTT	ACTOGCTCAC
6651	ATTTAATGTT	GATGAAAGCT	GGCTACAGGA	AGGOCAGAOG	CGAATTATTT
6701	TTGATGGOGT	TOCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA
6751	ACGOGAATTT	TAACAAAATA	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT
6801	ACAATCTTOC	TGTTTTTGGG	GCTTTTCTGA	TTATCAACOG	GGGTACATAT
6851	GATTGACATG	CTAGTTTTAC	GATTACCGTT	CATCGATTCT	CTTGTTTGCT
6901	CCAGACTCTC	AGGCAATGAC	CTGATAGOCT	TTGTAGATCT	CTCAAAAATA
6951	GCTAOCCTCT	COGGCATGAA	TTTATCAGCT	AGAAOGGTTG	AATATCATAT
7001	TGATGGTGAT	TTGACTGTCT	COGGCOCTTC	TCACOCCTTT	GAATCTTTAC
7051	CTACACATTA	CTCAGGCATT	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT
7101	TTTTATCCTT	GOGTTGAAAT	AAAGGCTTCT	COOGCAAAAG	TATTACAGGG
7151	TCATAATGTT	TTTGGTACAA	COGATTTAGC	TTTATGCTCT	GAGGCTTTAT

Figure 5

M13mp18 Nucleic Acid Sequence

11/23

COMPLEMENTARY TO M₁₃

POSITION	5' * 3'	POSITION	
645	AGCAACACTATCATA	631	M ₁₃ /1
615	ACGAOGATAAAAAOC	601	M ₁₃ /2
585	TTTTGCAAAAGAAGT	571	M ₁₃ /3
555	AATAGTAAATGTTT	541	M ₁₃ /4
525	CAATACTGOGGAATG	511	M ₁₃ /5
495	TGAATCCCCCTCAAA	481	M ₁₃ /6
465	AGAAAACGAGAATGA	451	M ₁₃ /7
435	CAGGTCTTTAOCCTG	421	M ₁₃ /8
405	AGGAAAGOGGATTGC	391	M ₁₃ /9
375	AGGAAGCCCGAAAGA	361	M ₁₃ /10

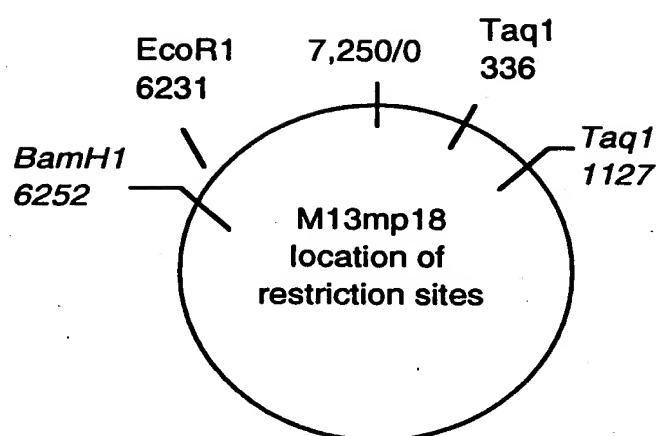
COMPLEMENTARY TO SS PHAGE DNA

POSITION	5' * 3'	POSITION	
351	ATATTTGAAGTCTTT	366	M ₁₃ /11
371	TCTTTTGTATGCAAT	386	M ₁₃ /12
391	CTATAATACTCAGGG	406	M ₁₃ /13
411	TGATTTATGGTCATT	426	M ₁₃ /14
431	GTTTAAAGCATTGA	446	M ₁₃ /15
451	TATTTATGACGATTC	466	M ₁₃ /16
471	TATCCAGTCTAAACA	486	M ₁₃ /17
491	CTCTGGCAAACTTC	506	M ₁₃ /18
511	TCGCTATTTTGGTTT	526	M ₁₃ /19
531	AAACGAGGGTTATGA	546	M ₁₃ /20

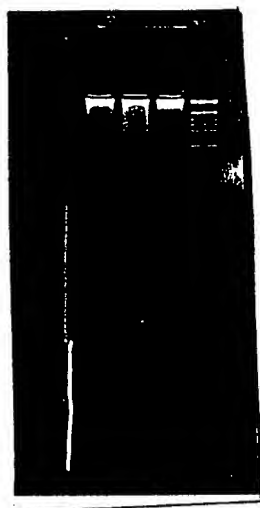
Figure 6

Primers for Nucleic Acid Production
Derived from M₁₃mp18 Sequence

12/23

**Figure 7****Appropriate M13mp18 Restriction Sites**

13/23



Lane 1: from calf thymus + Taq digested mp18 amplification reaction
Lane 2: from Taq digested mp18 amplification reaction
Lane 3: from calf thymus amplification reaction
Lane 4: øX174 Hinf1 size marker

Figure 8

14/23



Lane 1: no template

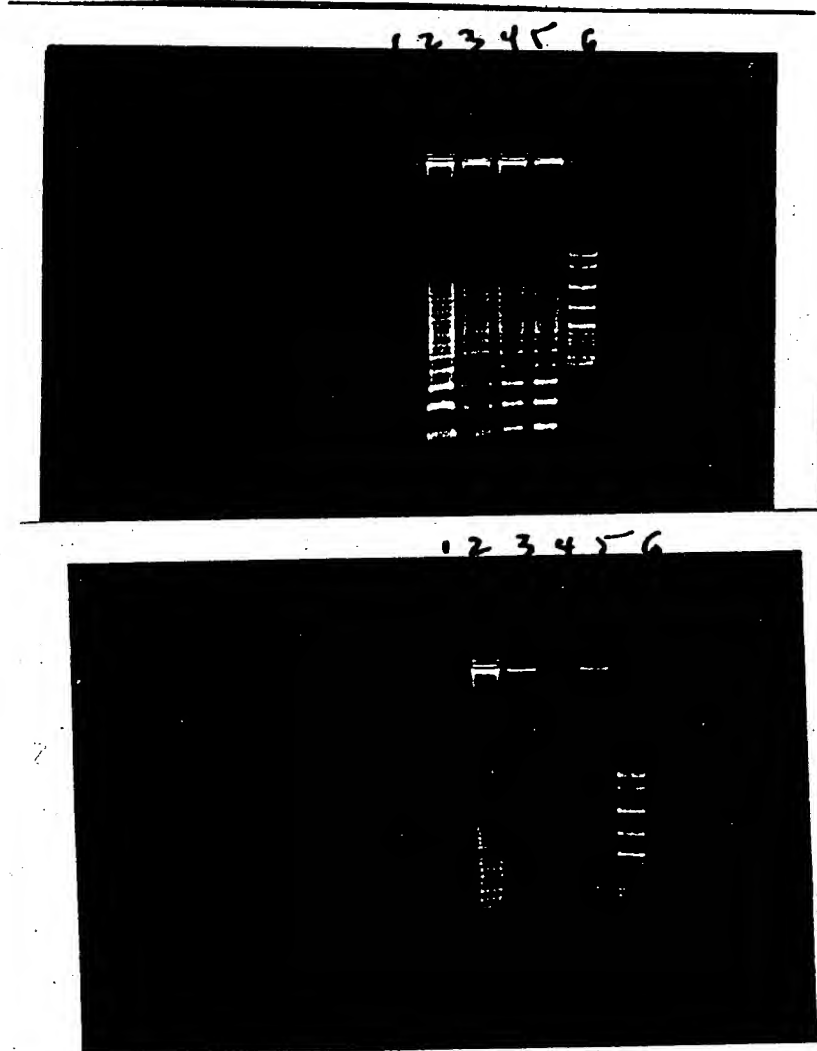
Lane 2: mp18 template, phosphate buffer

Lane 3: MspI/pBR322 size marker

Lane 4: mp18 template, MOPS buffer

Figure 9

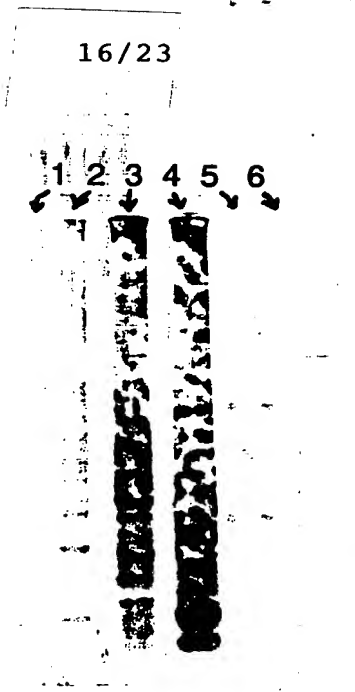
15/23



Top= (+) Template
Bottom= (-) Template

Lane 1: phosphate buffer
Lane 2: MES
Lane 3: MOPS
Lane 4: DMAB
Lane 5: DMG
Lane 6: pBR322/Mspl size marker

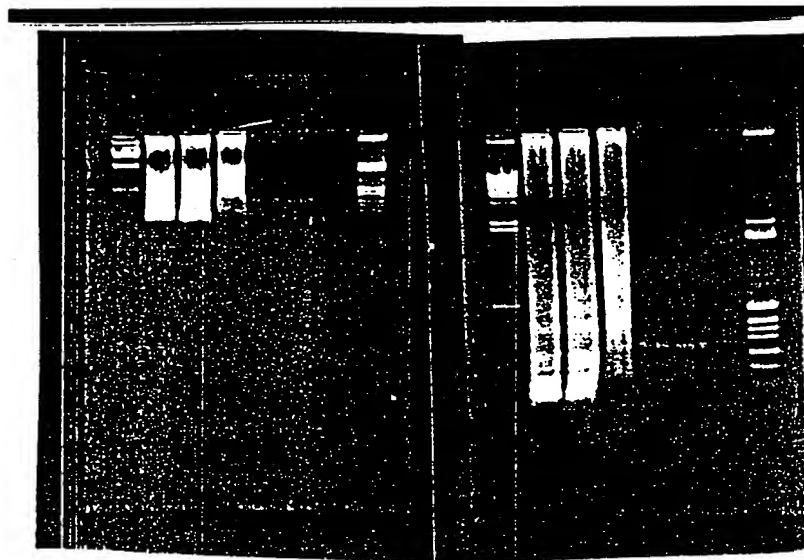
Figure 10



Lane 1: DMAB buffer, no template
Lane 2: DMAB buffer, mp18 template
Lane 3: DMG buffer, no template
Lane 4: DMG buffer, mp18 template
Lane 5: No reaction
Lane 6: 200 ng Taq I digested mp18
size marker/positive control

Figure 11

17/23



First Time Interval Second Time Interval

Agarose Gel Analysis

Lane 1: lambda Hind III marker
Lane 2: Amp/Untreated
Lane 3: Amp/Kinased
Lane 4: Amp/Kinased/Ligated
Lane 5: PCR/Untreated
Lane 6: PCR/Kinased
Lane 7: PCR/Kinased/Ligated
Lane 8: øX174/Hinf1 marker

Figure 12

18/23

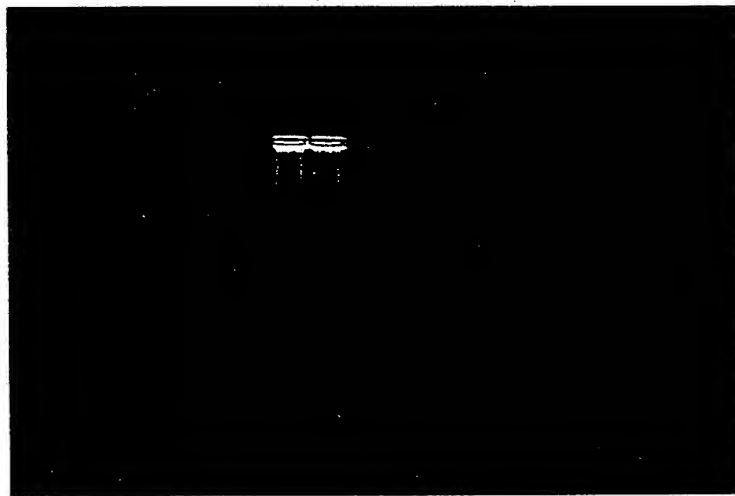
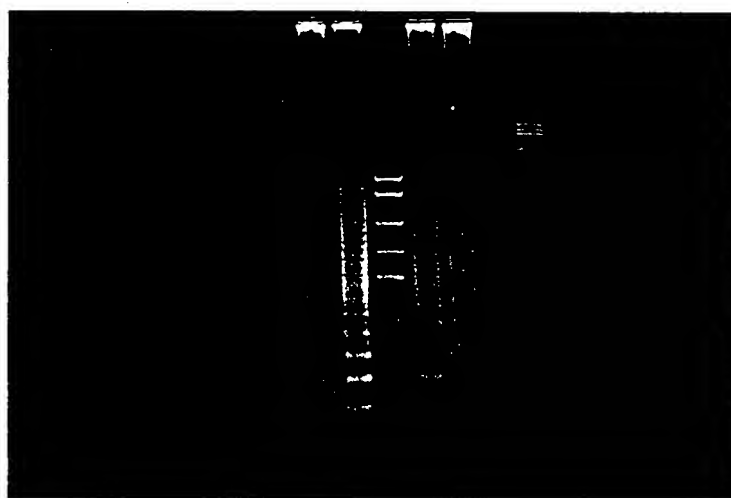


Figure 13

19/23

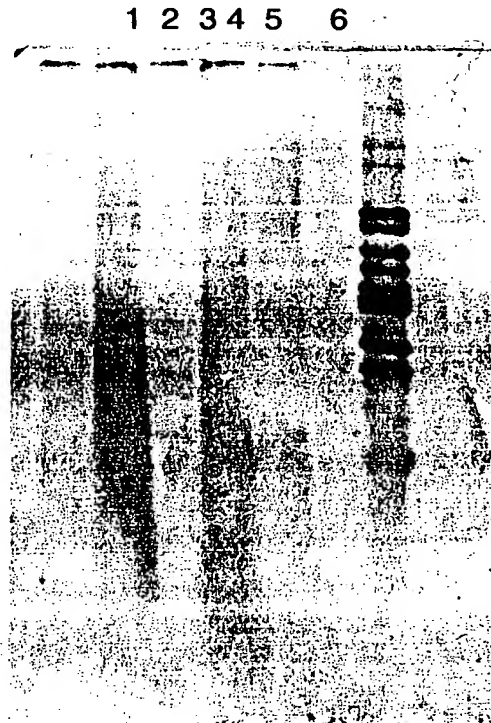
1 2 3 4 5 6



Lane 1: Primers alone
Lane 2: Primers + taq digested M13 DNA
Lane 3: Molecular weight markers
Lane 4: Primers + RNA
Lane 5: Primers alone
Lane 6: M13 digested DNA
Buffer was dimethyl amino glycine, pH 8.6

Figure 14

20/23



Lane 1: Primers alone
Lane 2: Primers + taq digested M13 DNA
Lane 3: Molecular weight markers
Lane 4: Primers + RNA
Lane 5: Primers alone
Lane 6: M13 digested DNA
Buffer was dimethyl amino glycine, pH 8.6

Figure 15

21/23

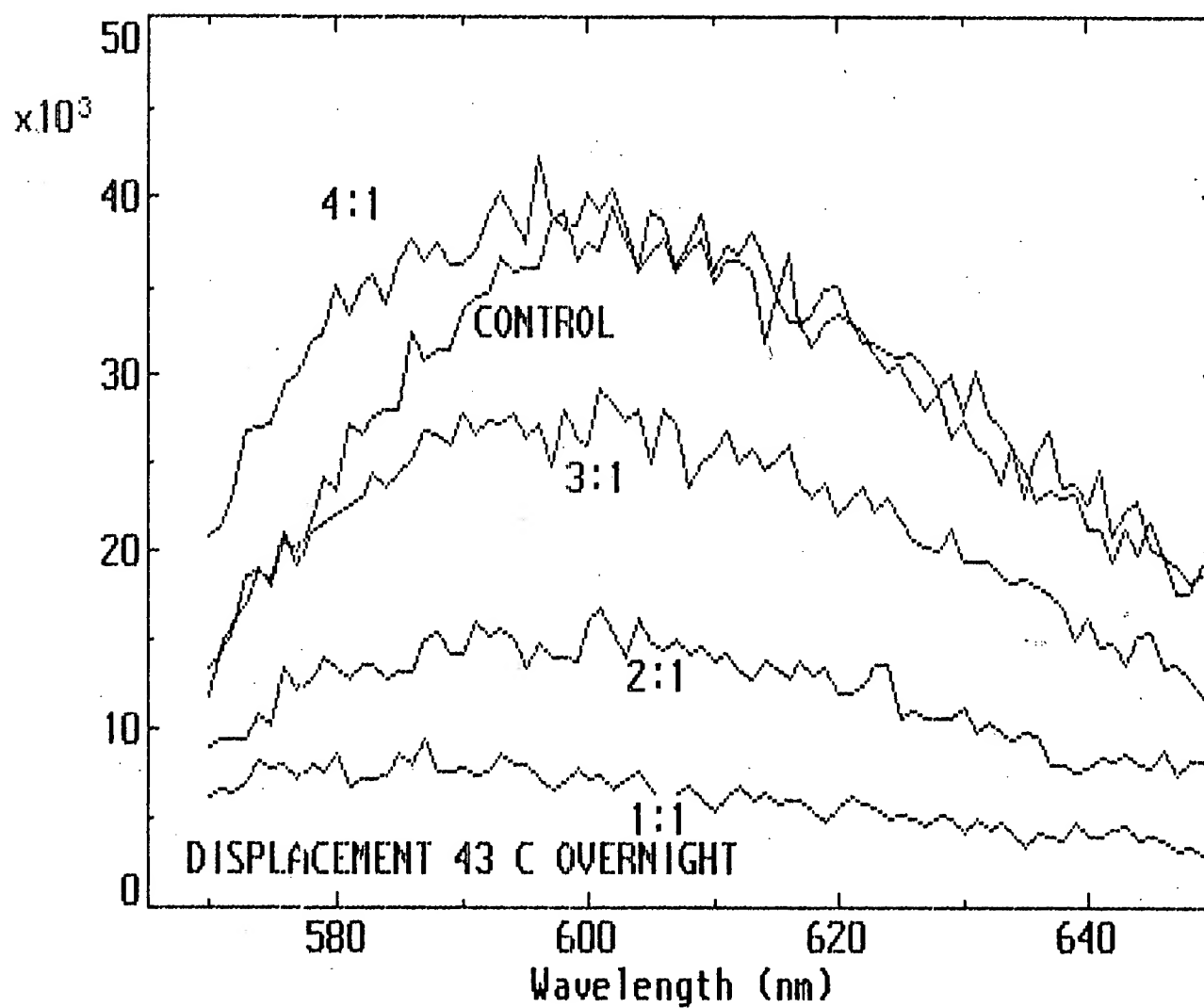


Figure 16

22/23

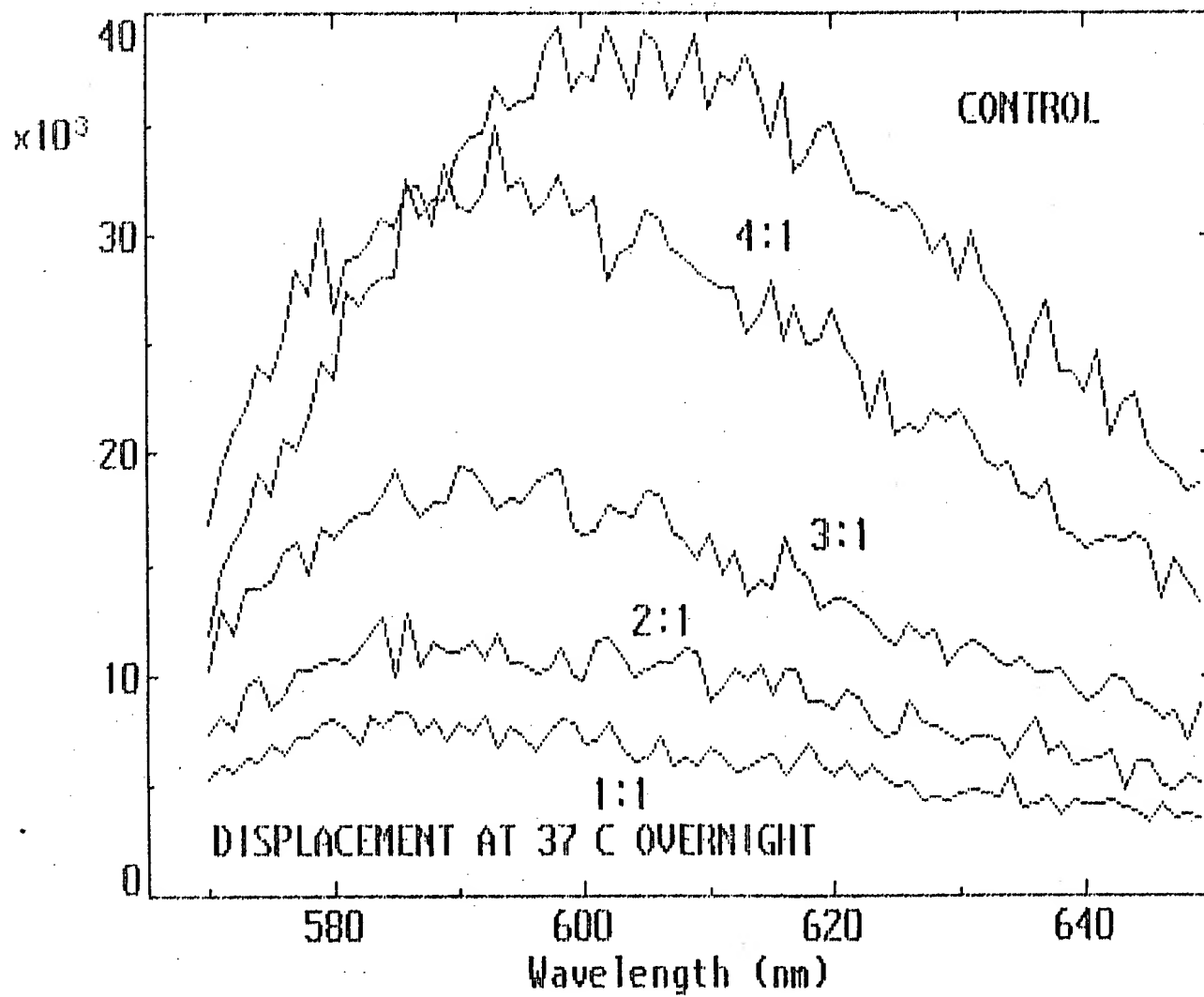


Figure 17

23/23

pIBI 31-BH5-2

fmet AUG of Lac z {T7 Promotor region....
 LAC PROMOTOR..ATG ACC ATG ATT ACG CCA GAT ATC AAA TTA ATA CGA CTC ACT ATA
 oligo 50-mer 3'- tac t*aa t*gc ggt* ct*a t*ag t*Vt aat* tat* gct* gag t*ga t*at* c-5'
 10 base insert

T7 RNA Start {« T3 Promotor Region }
 IGGG CTC ICCT TTA GTG ACG GTT AAT
 ...»} «- T3 Start Signal

pIBI 31 BSII/HCV

fmet AUG of Lac z {T3 Promotor region ->} T3 RNA Start
 LAC PROMOTOR ..ATG ACC ATG ATT ACG CCA AGC TCG AAA TTA ACC CTC ACT AAA /GGG
 oligo 50-mer 3'- tac t*aa t*ac t*aa t*gc ggt* t*V--10 base insert--.....

{«- T7 Promotor Region }
 MULTIPLE CLONING SITE + 390 BASE INSERT CTA /TAG TGA GTC CGT ATT AAT....
 «- T7 Start Signal
 5'-ct*a t*ag t*ga gt*c gt*a tt*a at*.....

Figure 18